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SEQUENCE LISTING

<110> TOJI, SHINGO
YANO, MINORU
TAMAI, KATSUYUKI

<120> THIOREDOXIN REDUCTASE II

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<140> 09/830,706

<141> 2001-04-27

<150> PCT/JP99/05983

<151> 1999-10-28

<150> JP 1998-310422

<151> 1998-10-30

<160> 38

<170> PatentIn Ver. 2.1

<210> 1

<211> 1959

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (10)..(1572)

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<221> misc_feature

<222> (1567)..(1569)

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10

cgg acg cag gcc gtg gcg ggc ggg gtg cgg ggc gcg gcg cgg ggc gca 99

Arg Thr Gln Ala Val Ala Gly Gly Val Arg Gly Ala Ala Arg Gly Ala

15

20

25

30

gca gca ggt cag cgg gac tat gat ctc ctg gtg gtc ggc ggg gga tct 147

Ala Ala Gly Gln Arg Asp Tyr Asp Leu Leu Val Val Gly Gly Gly Ser

35

40

45

ggt ggc ctg gct tgt gcc aag gag gcc gcc cag ctg gga agg aag gtg 195

Gly Gly Leu Ala Cys Ala Lys Glu Ala Ala Gln Leu Gly Arg Lys Val

50

55

60

gcc gtg gtg gac tac gtg gaa cct tct ccc caa ggc acc cgg tgg ggc 243

Ala Val Val Asp Tyr Val Glu Pro Ser Pro Gln Gly Thr Arg Trp Gly

65					70					75						
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Leu	Gly	Gly	Thr	Cys	Val	Asn	Val	Gly	Cys	Ile	Pro	Lys	Lys	Leu	Met	
80					85					90						
cac	cag	gcg	gca	ctg	ctg	gga	ggc	ctg	atc	caa	gat	gcc	ccc	aac	tat	339
His	Gln	Ala	Ala	Leu	Leu	Gly	Gly	Leu	Ile	Gln	Asp	Ala	Pro	Asn	Tyr	
95					100					105					110	
ggc	tgg	gag	gtg	gcc	cag	ccc	gtg	ccg	cat	gac	tgg	agg	aag	atg	gca	387
Gly	Trp	Glu	Val	Ala	Gln	Pro	Val	Pro	His	Asp	Trp	Arg	Lys	Met	Ala	
115					120					125						
gaa	gct	gtt	caa	aat	cac	gtg	aaa	tcc	ttg	aac	tgg	ggc	cac	cgt	gtc	435
Glu	Ala	Val	Gln	Asn	His	Val	Lys	Ser	Leu	Asn	Trp	Gly	His	Arg	Val	
130					135					140						
cag	ctt	cag	gac	aga	aaa	gtc	aag	tac	ttt	aac	atc	aaa	gcc	agc	ttt	483
Gln	Leu	Gln	Asp	Arg	Lys	Val	Lys	Tyr	Phe	Asn	Ile	Lys	Ala	Ser	Phe	
145					150					155						
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Val	Asp	Glu	His	Thr	Val	Cys	Gly	Val	Ala	Lys	Gly	Gly	Lys	Glu	Ile	
160					165					170						
ctg	ctg	tca	gcc	gat	cac	atc	atc	att	gct	act	gga	ggg	cgg	ccg	aga	579
Leu	Leu	Ser	Ala	Asp	His	Ile	Ile	Ile	Ala	Thr	Gly	Gly	Arg	Pro	Arg	
175					180					185					190	
tac	ccc	acg	cac	atc	gaa	ggt	gcc	ttg	gaa	tat	gga	atc	aca	agt	gat	627
Tyr	Pro	Thr	His	Ile	Glu	Gly	Ala	Leu	Glu	Tyr	Gly	Ile	Thr	Ser	Asp	
195					200					205						
gac	atc	ttc	tgg	ctg	aag	gaa	tcc	cct	gga	aaa	acg	ttg	gtg	gtc	ggg	675
Asp	Ile	Phe	Trp	Leu	Lys	Glu	Ser	Pro	Gly	Lys	Thr	Leu	Val	Val	Gly	
210					215					220						
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Ala	Ser	Tyr	Val	Ala	Leu	Glu	Cys	Ala	Gly	Phe	Leu	Thr	Gly	Ile	Gly	
225					230					235						
ctg	gac	acc	acc	atc	atg	atg	cgc	agc	atc	ccc	ctc	cgc	ggc	ttc	gac	771
Leu	Asp	Thr	Thr	Ile	Met	Met	Arg	Ser	Ile	Pro	Leu	Arg	Gly	Phe	Asp	
240					245					250						
cag	caa	atg	tcc	tcc	atg	gtc	ata	gag	cac	atg	gca	tct	cat	ggc	acc	819
Gln	Gln	Met	Ser	Ser	Met	Val	Ile	Glu	His	Met	Ala	Ser	His	Gly	Thr	
255					260					265					270	
cgg	ttc	ctg	agg	ggc	tgt	gcc	ccc	tcg	cgg	gtc	agg	agg	ctc	cct	gat	867
Arg	Phe	Leu	Arg	Gly	Cys	Ala	Pro	Ser	Arg	Val	Arg	Arg	Leu	Pro	Asp	
275					280					285						
ggc	cag	ctg	cag	gtc	acc	tgg	gag	gac	agc	acc	acc	ggc	aag	gag	gac	915
Gly	Gln	Leu	Gln	Val	Thr	Trp	Glu	Asp	Ser	Thr	Thr	Gly	Lys	Glu	Asp	
290					295					300						

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Thr Gly Thr Phe Asp Thr Val Leu Trp Ala Ile Gly Arg Val Pro Asp	
305 310 315	
acc aga agt ctg aat ttg gag aag gct ggg gta gat act agc ccc gac	1011
Thr Arg Ser Leu Asn Leu Glu Lys Ala Gly Val Asp Thr Ser Pro Asp	
320 325 330	
act cag aag atc ctg gtg gac tcc cgg gaa gcc acc tct gtg ccc cac	1059
Thr Gln Lys Ile Leu Val Asp Ser Arg Glu Ala Thr Ser Val Pro His	
335 340 345 350	
atc tac gcc att ggt gac gtg gtg gag ggg cgg cct gag ctg aca ccc	1107
Ile Tyr Ala Ile Gly Asp Val Val Glu Gly Arg Pro Glu Leu Thr Pro	
355 360 365	
aca gcg atc atg gcc ggg agg ctc ctg gtg cag cgg ctc ttc ggc ggg	1155
Thr Ala Ile Met Ala Gly Arg Leu Leu Val Gln Arg Leu Phe Gly Gly	
370 375 380	
tcc tca gat ctg atg gac tac gac aat gtt ccc acg acc gtc ttc acc	1203
Ser Ser Asp Leu Met Asp Tyr Asp Asn Val Pro Thr Thr Val Phe Thr	
385 390 395	
cca ctg gag tat ggc tgt gtg ggg ctg tcc gag gag gag gca gtg gct	1251
Pro Leu Glu Tyr Gly Cys Val Gly Leu Ser Glu Glu Glu Ala Val Ala	
400 405 410	
cgc cac ggg cag gag cat gtt gag gtc tat cac gcc cat tat aaa cca	1299
Arg His Gly Gln Glu His Val Glu Val Tyr His Ala His Tyr Lys Pro	
415 420 425 430	
ctg gag ttc acg gtg gct gga cga gat gca tcc cag tgt tat gta aag	1347
Leu Glu Phe Thr Val Ala Gly Arg Asp Ala Ser Gln Cys Tyr Val Lys	
435 440 445	
atg gtg tgc ctg agg gag ccc cca cag ctg gtg ctg ggc ctg cat ttc	1395
Met Val Cys Leu Arg Glu Pro Pro Gln Leu Val Leu Gly Leu His Phe	
450 455 460	
ctt ggc ccc aac gca ggc gaa gtt act caa gga ttt gct ctg ggg atc	1443
Leu Gly Pro Asn Ala Gly Glu Val Thr Gln Gly Phe Ala Leu Gly Ile	
465 470 475	
aag tgt ggg gct tcc tat gcg cag gtg atg cgg acc gtg ggt atc cat	1491
Lys Cys Gly Ala Ser Tyr Ala Gln Val Met Arg Thr Val Gly Ile His	
480 485 490	
ccc aca tgc tct gag gag gta gtc aag ctg cgc atc tcc aag cgc tca	1539
Pro Thr Cys Ser Glu Glu Val Val Lys Leu Arg Ile Ser Lys Arg Ser	
495 500 505 510	
ggc ctg gac ccc acg gtg aca ggc tgc tga ggg taagcgccat ccctgcaggc	1592
Gly Leu Asp Pro Thr Val Thr Gly Cys Xaa Gly	
515 520	

cagggcacac ggtgcgcccc cgcagctc ctcggaggcc agaccagga tggctgcagg 1652
ccaggtttgg ggggcctcaa cctctcctg gagcgctgt gagatgggtca gcgtggagcg 1712
caagtgtg acgggtggcc cgtgtgcccc acagggatgg ctcaggggac tgtccacctc 1772
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aaaaaaaa 1959

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<213> Homo sapiens

<220>
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<222> (520)
<223> Selenocysteine

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Gly Gln Arg Asp Tyr Asp Leu Leu Val Val Gly Gly Gly Ser Gly Gly
35 40 45
Leu Ala Cys Ala Lys Glu Ala Ala Gln Leu Gly Arg Lys Val Ala Val
50 55 60
Val Asp Tyr Val Glu Pro Ser Pro Gln Gly Thr Arg Trp Gly Leu Gly
65 70 75 80
Gly Thr Cys Val Asn Val Gly Cys Ile Pro Lys Lys Leu Met His Gln
85 90 95
Ala Ala Leu Leu Gly Gly Leu Ile Gln Asp Ala Pro Asn Tyr Gly Trp
100 105 110
Glu Val Ala Gln Pro Val Pro His Asp Trp Arg Lys Met Ala Glu Ala
115 120 125
Val Gln Asn His Val Lys Ser Leu Asn Trp Gly His Arg Val Gln Leu
130 135 140
Gln Asp Arg Lys Val Lys Tyr Phe Asn Ile Lys Ala Ser Phe Val Asp
145 150 155 160
Glu His Thr Val Cys Gly Val Ala Lys Gly Gly Lys Glu Ile Leu Leu

165										170					175						
Ser	Ala	Asp	His	Ile	Ile	Ile	Ala	Thr	Gly	Gly	Arg	Pro	Arg	Tyr	Pro						
			180					185					190								
Thr	His	Ile	Glu	Gly	Ala	Leu	Glu	Tyr	Gly	Ile	Thr	Ser	Asp	Asp	Ile						
		195					200					205									
Phe	Trp	Leu	Lys	Glu	Ser	Pro	Gly	Lys	Thr	Leu	Val	Val	Gly	Ala	Ser						
	210					215					220										
Tyr	Val	Ala	Leu	Glu	Cys	Ala	Gly	Phe	Leu	Thr	Gly	Ile	Gly	Leu	Asp						
225					230					235					240						
Thr	Thr	Ile	Met	Met	Arg	Ser	Ile	Pro	Leu	Arg	Gly	Phe	Asp	Gln	Gln						
			245						250					255							
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			260					265					270								
Leu	Arg	Gly	Cys	Ala	Pro	Ser	Arg	Val	Arg	Arg	Leu	Pro	Asp	Gly	Gln						
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Leu	Gln	Val	Thr	Trp	Glu	Asp	Ser	Thr	Thr	Gly	Lys	Glu	Asp	Thr	Gly						
	290					295					300										
Thr	Phe	Asp	Thr	Val	Leu	Trp	Ala	Ile	Gly	Arg	Val	Pro	Asp	Thr	Arg						
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Ser	Leu	Asn	Leu	Glu	Lys	Ala	Gly	Val	Asp	Thr	Ser	Pro	Asp	Thr	Gln						
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Lys	Ile	Leu	Val	Asp	Ser	Arg	Glu	Ala	Thr	Ser	Val	Pro	His	Ile	Tyr						
		340					345						350								
Ala	Ile	Gly	Asp	Val	Val	Glu	Gly	Arg	Pro	Glu	Leu	Thr	Pro	Thr	Ala						
		355					360					365									
Ile	Met	Ala	Gly	Arg	Leu	Leu	Val	Gln	Arg	Leu	Phe	Gly	Gly	Ser	Ser						
	370					375					380										
Asp	Leu	Met	Asp	Tyr	Asp	Asn	Val	Pro	Thr	Thr	Val	Phe	Thr	Pro	Leu						
385					390					395					400						
Glu	Tyr	Gly	Cys	Val	Gly	Leu	Ser	Glu	Glu	Glu	Ala	Val	Ala	Arg	His						
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Gly	Gln	Glu	His	Val	Glu	Val	Tyr	His	Ala	His	Tyr	Lys	Pro	Leu	Glu						
			420					425					430								
Phe	Thr	Val	Ala	Gly	Arg	Asp	Ala	Ser	Gln	Cys	Tyr	Val	Lys	Met	Val						
		435					440					445									
Cys	Leu	Arg	Glu	Pro	Pro	Gln	Leu	Val	Leu	Gly	Leu	His	Phe	Leu	Gly						
	450					455					460										
Pro	Asn	Ala	Gly	Glu	Val	Thr	Gln	Gly	Phe	Ala	Leu	Gly	Ile	Lys	Cys						

465		470		475		480									
Gly	Ala	Ser	Tyr	Ala	Gln	Val	Met	Arg	Thr	Val	Gly	Ile	His	Pro	Thr
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Cys	Ser	Glu	Glu	Val	Val	Lys	Leu	Arg	Ile	Ser	Lys	Arg	Ser	Gly	Leu
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 <222> (188)..(1669)

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 <222> (1664)..(1666)
 <223> "tga" is translated to selenocysteine

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 agtagacacg atgacacctt ttgcaggcta aaaaggctga gaggggcact atgtgcagtg 180
 agccacc atg gag gac caa gca ggt cag cgg gac tat gat ctc ctg gtg 229
 Met Glu Asp Gln Ala Gly Gln Arg Asp Tyr Asp Leu Leu Val
 1 5 10
 gtc ggc ggg gga tct ggt ggc ctg gct tgt gcc aag gag gcc gcc cag 277
 Val Gly Gly Gly Ser Gly Gly Leu Ala Cys Ala Lys Glu Ala Ala Gln
 15 20 25 30
 ctg gga agg aag gtg gcc gtg gtg gac tac gtg gaa cct tct ccc caa 325
 Leu Gly Arg Lys Val Ala Val Val Asp Tyr Val Glu Pro Ser Pro Gln
 35 40 45
 ggc acc cgg tgg ggc ctc ggc ggc acc tgc gtc aac gtg ggc tgc atc 373
 Gly Thr Arg Trp Gly Leu Gly Gly Thr Cys Val Asn Val Gly Cys Ile
 50 55 60
 ccc aag aag ctg atg cac cag gcg gca ctg ctg gga ggc ctg atc caa 421
 Pro Lys Lys Leu Met His Gln Ala Ala Leu Leu Gly Gly Leu Ile Gln
 65 70 75
 gat gcc ccc aac tat ggc tgg gag gtg gcc cag ccc gtg ccg cat gac 469
 Asp Ala Pro Asn Tyr Gly Trp Glu Val Ala Gln Pro Val Pro His Asp
 80 85 90

tgg agg aag atg gca gaa gct gtt caa aat cac gtg aaa tcc ttg aac	517
Trp Arg Lys Met Ala Glu Ala Val Gln Asn His Val Lys Ser Leu Asn	
95 100 105 110	
tgg ggc cac cgt gtc cag ctt cag gac aga aaa gtc aag tac ttt aac	565
Trp Gly His Arg Val Gln Leu Gln Asp Arg Lys Val Lys Tyr Phe Asn	
115 120 125	
atc aaa gcc agc ttt gtt gac gag cac acg gtt tgc ggc gtt gcc aaa	613
Ile Lys Ala Ser Phe Val Asp Glu His Thr Val Cys Gly Val Ala Lys	
130 135 140	
ggg ggg aaa gag att ctg ctg tca gcc gat cac atc atc att gct act	661
Gly Gly Lys Glu Ile Leu Leu Ser Ala Asp His Ile Ile Ile Ala Thr	
145 150 155	
gga ggg cgg ccg aga tac ccc acg cac atc gaa ggt gcc ttg gaa tat	709
Gly Gly Arg Pro Arg Tyr Pro Thr His Ile Glu Gly Ala Leu Glu Tyr	
160 165 170	
gga atc aca agt gat gac atc ttc tgg ctg aag gaa tcc cct gga aaa	757
Gly Ile Thr Ser Asp Asp Ile Phe Trp Leu Lys Glu Ser Pro Gly Lys	
175 180 185 190	
acg ttg gtg gtc ggg gcc agc tat gtg gcc ctg gag tgt gct ggc ttc	805
Thr Leu Val Val Gly Ala Ser Tyr Val Ala Leu Glu Cys Ala Gly Phe	
195 200 205	
ctc acc ggg att ggg ctg gac acc acc atc atg atg cgc agc atc ccc	853
Leu Thr Gly Ile Gly Leu Asp Thr Thr Ile Met Met Arg Ser Ile Pro	
210 215 220	
ctc cgc ggc ttc gac cag caa atg tcc tcc atg gtc ata gag cac atg	901
Leu Arg Gly Phe Asp Gln Gln Met Ser Ser Met Val Ile Glu His Met	
225 230 235	
gca tct cat ggc acc cgg ttc ctg agg ggc tgt gcc ccc tcg cgg gtc	949
Ala Ser His Gly Thr Arg Phe Leu Arg Gly Cys Ala Pro Ser Arg Val	
240 245 250	
agg agg ctc cct gat ggc cag ctg cag gtc acc tgg gag gac agc acc	997
Arg Arg Leu Pro Asp Gly Gln Leu Gln Val Thr Trp Glu Asp Ser Thr	
255 260 265 270	
acc ggc aag gag gac acg ggc acc ttt gac acc gtc ctg tgg gcc ata	1045
Thr Gly Lys Glu Asp Thr Gly Thr Phe Asp Thr Val Leu Trp Ala Ile	
275 280 285	
ggg cga gtc cca gac acc aga agt ctg aat ttg gag aag gct ggg gta	1093
Gly Arg Val Pro Asp Thr Arg Ser Leu Asn Leu Glu Lys Ala Gly Val	
290 295 300	
gat act agc ccc gac act cag aag atc ctg gtg gac tcc cgg gaa gcc	1141
Asp Thr Ser Pro Asp Thr Gln Lys Ile Leu Val Asp Ser Arg Glu Ala	
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<213> Homo sapiens

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<222> (493)
<223> Selenocysteine

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			20				25						30		
Arg	Lys	Val	Ala	Val	Val	Asp	Tyr	Val	Glu	Pro	Ser	Pro	Gln	Gly	Thr
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Arg	Trp	Gly	Leu	Gly	Gly	Thr	Cys	Val	Asn	Val	Gly	Cys	Ile	Pro	Lys
	50					55					60				
Lys	Leu	Met	His	Gln	Ala	Ala	Leu	Leu	Gly	Gly	Leu	Ile	Gln	Asp	Ala
65					70					75					80
Pro	Asn	Tyr	Gly	Trp	Glu	Val	Ala	Gln	Pro	Val	Pro	His	Asp	Trp	Arg
				85					90					95	
Lys	Met	Ala	Glu	Ala	Val	Gln	Asn	His	Val	Lys	Ser	Leu	Asn	Trp	Gly
		100						105					110		
His	Arg	Val	Gln	Leu	Gln	Asp	Arg	Lys	Val	Lys	Tyr	Phe	Asn	Ile	Lys
		115					120					125			
Ala	Ser	Phe	Val	Asp	Glu	His	Thr	Val	Cys	Gly	Val	Ala	Lys	Gly	Gly
		130					135					140			
Lys	Glu	Ile	Leu	Leu	Ser	Ala	Asp	His	Ile	Ile	Ile	Ala	Thr	Gly	Gly
145						150				155					160
Arg	Pro	Arg	Tyr	Pro	Thr	His	Ile	Glu	Gly	Ala	Leu	Glu	Tyr	Gly	Ile
				165					170					175	
Thr	Ser	Asp	Asp	Ile	Phe	Trp	Leu	Lys	Glu	Ser	Pro	Gly	Lys	Thr	Leu
			180					185					190		
Val	Val	Gly	Ala	Ser	Tyr	Val	Ala	Leu	Glu	Cys	Ala	Gly	Phe	Leu	Thr
			195					200					205		
Gly	Ile	Gly	Leu	Asp	Thr	Thr	Ile	Met	Met	Arg	Ser	Ile	Pro	Leu	Arg
	210					215					220				
Gly	Phe	Asp	Gln	Gln	Met	Ser	Ser	Met	Val	Ile	Glu	His	Met	Ala	Ser
225					230						235				240

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 245 250 255
 Leu Pro Asp Gly Gln Leu Gln Val Thr Trp Glu Asp Ser Thr Thr Gly
 260 265 270
 Lys Glu Asp Thr Gly Thr Phe Asp Thr Val Leu Trp Ala Ile Gly Arg
 275 280 285
 Val Pro Asp Thr Arg Ser Leu Asn Leu Glu Lys Ala Gly Val Asp Thr
 290 295 300
 Ser Pro Asp Thr Gln Lys Ile Leu Val Asp Ser Arg Glu Ala Thr Ser
 305 310 315 320
 Val Pro His Ile Tyr Ala Ile Gly Asp Val Val Glu Gly Arg Pro Glu
 325 330 335
 Leu Thr Pro Thr Ala Ile Met Ala Gly Arg Leu Leu Val Gln Arg Leu
 340 345 350
 Phe Gly Gly Ser Ser Asp Leu Met Asp Tyr Asp Asn Val Pro Thr Thr
 355 360 365
 Val Phe Thr Pro Leu Glu Tyr Gly Cys Val Gly Leu Ser Glu Glu Glu
 370 375 380
 Ala Val Ala Arg His Gly Gln Glu His Val Glu Val Tyr His Ala His
 385 390 395 400
 Tyr Lys Pro Leu Glu Phe Thr Val Ala Gly Arg Asp Ala Ser Gln Cys
 405 410 415
 Tyr Val Lys Met Val Cys Leu Arg Glu Pro Pro Gln Leu Val Leu Gly
 420 425 430
 Leu His Phe Leu Gly Pro Asn Ala Gly Glu Val Thr Gln Gly Phe Ala
 435 440 445
 Leu Gly Ile Lys Cys Gly Ala Ser Tyr Ala Gln Val Met Arg Thr Val
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 Gly Ile His Pro Thr Cys Ser Glu Glu Val Val Lys Leu Arg Ile Ser
 465 470 475 480
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<210> 5

<211> 130

<212> DNA

<213> Homo sapiens

<400> 5

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aagagggtac 130

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<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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<210> 7
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 7
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<210> 8
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<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 8
tatgatctcc tggtggtc 18

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<220>
<223> Description of Artificial Sequence: Primer

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gtcatcactt gtgattcc 18

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<220>
 <223> Description of Artificial Sequence: Primer

 <400> 10
 acagcttctg ccatcttcct c 21

 <210> 11
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 <220>
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 <400> 11
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 <210> 12
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 <220>
 <223> Description of Artificial Sequence: Primer

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 <220>
 <223> Description of Artificial Sequence: Primer

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<211> 21
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<223> Description of Artificial Sequence: Primer

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<210> 18
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